

SEQUENCE LISTING

<110> Cases, Sylvaine
 Stone, Scot
 Zhou, Ping
 Farese, Robert V.
 Chi-Liang Eric Yen

<120> MONO- AND DIACYGLYCEROL ACYLTRANSFERASES AND METHODS OF USE THEREOF

<130> UCAL240CIP

<140> Unassigned
 <141> 2002-01-14

<150> 60/271,307
 <151> 2001-02-23

<150> 09/794,715
 <151> 2001-02-26

<160> 18

<170> FastSEQ for Windows Version 4.0

<210> 1
 <211> 1231
 <212> DNA
 <213> Homo sapiens

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 atggggcact ggatccagca tctctccgc cctccaggac ctcttctctg tcacctggct 180
 caataggtcc aagggtgaaa agcagctaca ggtcatctca gtgtccagt gggtcctgtc 240
 ctctcttgta ctgggagtgg cctgcagtgc catcctcatg tacatattct gcactgattg 300
 ctggctcatc gctgtgctct acttcacttg gctgggtgtt gactggaaca caccaagaa 360
 aggtggcagg aggtcacagt gggtcgaaa ctgggctgtg tggcgctact ttcgagacta 420
 ctttcccatc cagctgggtga agacacacaa cctgctgacc accaggaact atatctttgg 480
 ataccacccc catggtatca tgggcctggg tgccttctgc aacttcagca cagaggccac 540
 agaagtgage aagaagttcc caggcatacg gccttacctg gctacactgg caggcaactt 600
 ccgaatgcct gtgttgagg agtacctgat gtctggaggt atctgcctg tcagccggga 660
 caccatagac tatttgcttt caaagaatgg gagtggcaat gctatcatca tcgtggctcg 720
 ggggtgcggct gagtctctga gctccatgcc tggcaagaat gcagtcaccc tgcggaaccg 780
 caagggtctt gtgaaactgg cctgcgtca tggagctgac ctggttccca tctactcctt 840
 tggagagaat gaagtgtaca agcaggtgat cttcgaggag ggctcctggg gccgatgggt 900
 ccagaagaag ttccagaaat acattggttt cgcctcatgc atcttccatg gtcgaggcct 960
 cttctoctoc gacacctggg ggctgggtgcc ctactccaag cccatcacca ctgttggtgg 1020
 agagcccatc accatcccca agctggagca cccaaccag caagacatcg acctgtacca 1080
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caccatgtac atggaggccc tggatgaagct cttcgacaag cacaagacca agttcggcct 1140
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<210> 2
 <211> 388
 <212> PRT
 <213> Homo sapiens

<400> 2
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 Ser Arg Glu Gly Ser Gly Arg Trp Gly Thr Gly Ser Ser Ile Leu Ser
 35 40 45
 Ala Leu Gln Asp Leu Phe Ser Val Thr Trp Leu Asn Arg Ser Lys Val
 50 55 60
 Glu Lys Gln Leu Gln Val Ile Ser Val Leu Gln Trp Val Leu Ser Phe
 65 70 75 80
 Leu Val Leu Gly Val Ala Cys Ser Ala Ile Leu Met Tyr Ile Phe Cys
 85 90 95
 Thr Asp Cys Trp Leu Ile Ala Val Leu Tyr Phe Thr Trp Leu Val Phe
 100 105 110
 Asp Trp Asn Thr Pro Lys Lys Gly Gly Arg Arg Ser Gln Trp Val Arg
 115 120 125
 Asn Trp Ala Val Trp Arg Tyr Phe Arg Asp Tyr Phe Pro Ile Gln Leu
 130 135 140
 Val Lys Thr His Asn Leu Leu Thr Thr Arg Asn Tyr Ile Phe Gly Tyr
 145 150 155 160
 His Pro His Gly Ile Met Gly Leu Gly Ala Phe Cys Asn Phe Ser Thr
 165 170 175
 Glu Ala Thr Glu Val Ser Lys Lys Phe Pro Gly Ile Arg Pro Tyr Leu
 180 185 190
 Ala Thr Leu Ala Gly Asn Phe Arg Met Pro Val Leu Arg Glu Tyr Leu
 195 200 205
 Met Ser Gly Gly Ile Cys Pro Val Ser Arg Asp Thr Ile Asp Tyr Leu
 210 215 220
 Leu Ser Lys Asn Gly Ser Gly Asn Ala Ile Ile Ile Val Val Gly Gly
 225 230 235 240
 Ala Ala Glu Ser Leu Ser Ser Met Pro Gly Lys Asn Ala Val Thr Leu
 245 250 255
 Arg Asn Arg Lys Gly Phe Val Lys Leu Ala Leu Arg His Gly Ala Asp
 260 265 270
 Leu Val Pro Ile Tyr Ser Phe Gly Glu Asn Glu Val Tyr Lys Gln Val
 275 280 285
 Ile Phe Glu Glu Gly Ser Trp Gly Arg Trp Val Gln Lys Lys Phe Gln
 290 295 300
 Lys Tyr Ile Gly Phe Ala Pro Cys Ile Phe His Gly Arg Gly Leu Phe
 305 310 315 320
 Ser Ser Asp Thr Trp Gly Leu Val Pro Tyr Ser Lys Pro Ile Thr Thr

325 330 335
 Val Val Gly Glu Pro Ile Thr Ile Pro Lys Leu Glu His Pro Thr Gln
 340 345 350
 Gln Asp Ile Asp Leu Tyr His Thr Met Tyr Met Glu Ala Leu Val Lys
 355 360 365
 Leu Phe Asp Lys His Lys Thr Lys Phe Gly Leu Pro Glu Thr Glu Val
 370 375 380
 Leu Glu Val Asn
 385

<210> 3
 <211> 1167
 <212> DNA
 <213> Mus musculus

<220>
 <221> misc_feature
 <222> (1)...(1167)
 <223> n = A,T,C or G

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 ggcaactggc ccagcatcct ctcagccctc caagacatct tctctgtcac ctggctcaac 180
 agatcyaagg tggaaaaaca gctgcaggtc atctcagtac tacaatgggt cctatccttc 240
 ctggtgctag gaggggcctg cagtgtcatc ctcagtata ccttctgcac agactgctgg 300
 ctgatagctg tgctctactt cacctggctg gcatttgact ggaacacgcc caagaaaggt 360
 ggcaggagat cgcagtgggt gcgaaactgg gccgtgtggc gctacttccg agactacttt 420
 cccatccagc tgggtgaagac acacaacctg ctgaccacca ggaactatat ctttgggatac 480
 caccatccatg gcatcatggg cctgggtgcc ttctgtaact tcagcacaga ggctactgaa 540
 gtcagcaaga agtttctctg cataaggccc tatttggtta cgttggcygg taacttccgg 600
 atgcctgtgc ttgcgcagta cctgatgtct ggaggcatct gccctgtcaa ccgagacacc 660
 atagactact tgctctccaa gaatgggagt ggcaatgcta tcacatcgt ggtgggaggt 720
 gcagctgagt ccctgagctc catgcctggc aagaacgcag tcaccctgaa gaaccgcaa 780
 ggctttgtga agctggccct gcgccatgga gctgatctgg tccccactta ttcctttgga 840
 gagaatgagg tatacaagca ggtgatcttt gaggagggtt cctggggccg atgggtccag 900
 aagaagttcc agaagtatat tggtttcgcc ccctgcacat tccatggccg aggcctcttc 960
 tcctctgaca cctggggggt ggtgccctac tccaagccca tcaccaccgt cgtgggggag 1020
 cccatcactg tccccaaagt ggagcaccgc acccagaaag acatcgacct gtaccatgcc 1080
 atgtacatgg aggccctggg gaagctcttt gacaatcaca agaccaaatt tggcctncca 1140
 gagactgagg tgctggaggt gaactga 1167

<210> 4
 <211> 387
 <212> PRT
 <213> Mus musculus

<400> 4
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 Arg Ala Glu Leu Pro Ala Ala Lys Asn Lys Asn Lys Gly Ser Ala Leu

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Ser	Arg	Glu	Gly	Ser	Gly	Arg	Trp	Gly	Thr	Gly	Ser	Ser	Ile	Leu	Ser
35				40				45							
Ala	Leu	Gln	Asp	Ile	Phe	Ser	Val	Thr	Trp	Leu	Asn	Arg	Ser	Lys	Val
50				55				60							
Glu	Lys	Gln	Leu	Gln	Val	Ile	Ser	Val	Leu	Gln	Trp	Val	Leu	Ser	Phe
65	70				75				80						
Leu	Val	Leu	Gly	Val	Ala	Cys	Ser	Val	Ile	Leu	Met	Tyr	Thr	Phe	Cys
85				90				95							
Thr	Asp	Cys	Trp	Leu	Ile	Ala	Val	Leu	Tyr	Phe	Thr	Trp	Leu	Ala	Phe
100				105				110							
Asp	Trp	Asn	Thr	Pro	Lys	Lys	Gly	Gly	Arg	Arg	Ser	Gln	Trp	Val	Arg
115				120				125							
Asn	Trp	Ala	Val	Trp	Arg	Tyr	Phe	Arg	Asp	Tyr	Phe	Pro	Ile	Gln	Leu
130				135				140							
Val	Lys	Thr	His	Asn	Leu	Leu	Thr	Thr	Arg	Asn	Tyr	Ile	Phe	Gly	Tyr
145	150				155				160						
His	Pro	His	Gly	Ile	Met	Gly	Leu	Gly	Ala	Phe	Cys	Asn	Phe	Ser	Thr
165				170				175							
Glu	Ala	Thr	Glu	Val	Ser	Lys	Lys	Phe	Pro	Gly	Ile	Arg	Pro	Tyr	Leu
180				185				190							
Ala	Thr	Leu	Ala	Gly	Asn	Phe	Arg	Met	Pro	Val	Leu	Arg	Glu	Tyr	Leu
195				200				205							
Met	Ser	Gly	Gly	Ile	Cys	Leu	Val	Asn	Arg	Asp	Thr	Ile	Asp	Tyr	Leu
210				215				220							
Leu	Ser	Lys	Asn	Gly	Ser	Gly	Asn	Ala	Ile	Ile	Ile	Val	Val	Gly	Gly
225	230				235				240						
Ala	Ala	Glu	Ser	Leu	Ser	Ser	Met	Pro	Gly	Lys	Asn	Ala	Val	Thr	Leu
245				250				255							
Lys	Asn	Arg	Lys	Gly	Phe	Val	Lys	Leu	Ala	Leu	Arg	His	Gly	Ala	Asp
260				265				270							
Leu	Val	Pro	Thr	Tyr	Ser	Phe	Gly	Glu	Asn	Glu	Val	Tyr	Lys	Gln	Val
275				280				285							
Ile	Phe	Glu	Glu	Gly	Ser	Trp	Gly	Arg	Trp	Val	Lys	Lys	Phe	Gln	Lys
290				295				300							
Tyr	Ile	Gly	Phe	Ala	Pro	Cys	Ile	Phe	His	Gly	Arg	Gly	Leu	Phe	Ser
305	310				315				320						
Ser	Asp	Thr	Trp	Gly	Leu	Val	Pro	Tyr	Ser	Lys	Pro	Ile	Thr	Thr	Val
325				330				335							
Val	Gly	Glu	Pro	Ile	Thr	Val	Pro	Lys	Leu	Glu	His	Pro	Thr	Gln	Lys
340				345				350							
Asp	Ile	Asp	Leu	Tyr	His	Ala	Met	Tyr	Met	Glu	Ala	Leu	Val	Lys	Leu
355				360				365							
Phe	Asp	Asn	His	Lys	Thr	Lys	Phe	Gly	Leu	Pro	Glu	Thr	Glu	Val	Leu
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Glu	Val	Asn													
385															

<212> DNA

<213> Mus musculus

<400> 5

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atgtcgggtcc tgtacaacta ttggttcctt tacatcccat atctgggtctg gttttactat      180
gactggagaa ccccgagagca aggaggcaga agatggaact ggggtccaaag ctggcctgtg      240
tggaagtatt ttaaggagta ttttccaatc tgtcttgtca aaacgcagga tttggatccg      300
ggtcacaatt atatatttgg gtttcaccct catggaatat tcgtgcctgg agcctttgga      360
aatttttcta caaaatactc ggacttcaag aagctatttc ctggctttac atcgtatctc      420
cacgtggcca agatctgggt ctgtttcccg ttgttccgag aatatctgat gagtaacggg      480
ccggtttcag tgtctaagga gagtttgtct catgtgctga gcaaggatgg aggtggcaat      540
gtctcaatca ttgtcctcgg aggtgcaaag gaggcgctgg aggtcaccac aggaacattc      600
accctgtgca tccgccagcg caaagggttt gttaagatgg ccttgaccca tgggtgccagt      660
ttggttccag tattttcttt tgggtgaaaat gatctatata agcaaattaa caaccccaaa      720
ggctcctggc tacgaactat acaagacgca atgtatgatt caatgggagt agccttgcca      780
ctgatataat ccagaggaat tttccagcac tactttggca taatgcccta tcggaagctg      840
atctacactg ttgttggccg ccctatccct gtccagcaga ttctgaaccc gacctcagag      900
cagattgaag agctgcacga gacataccta gaggagctaa agaaactatt caatgaacac      960
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<210> 6

<211> 335

<212> PRT

<213> Mus musculus

<400> 6

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      20             25             30
Gln Val Cys Ile Gly Ile Met Val Met Leu Val Leu Tyr Asn Tyr Trp
      35             40             45
Phe Leu Tyr Ile Pro Tyr Leu Val Trp Phe Tyr Tyr Asp Trp Arg Thr
      50             55             60
Pro Glu Gln Gly Gly Arg Arg Trp Asn Trp Val Gln Ser Trp Pro Val
      65             70             75             80
Trp Lys Tyr Phe Lys Glu Tyr Phe Pro Ile Cys Leu Val Lys Thr Gln
      85             90             95
Asp Leu Asp Pro Gly His Asn Tyr Ile Phe Gly Phe His Pro His Gly
      100            105            110
Ile Phe Val Pro Gly Ala Phe Gly Asn Phe Cys Thr Lys Tyr Ser Asp
      115            120            125
Phe Lys Lys Leu Phe Pro Gly Phe Thr Ser Tyr Leu His Val Ala Lys
      130            135            140
Ile Trp Phe Cys Phe Pro Leu Phe Arg Glu Tyr Leu Met Ser Asn Gly
      145            150            155            160
Pro Val Ser Val Ser Lys Glu Ser Leu Ser His Val Leu Ser Lys Asp
      165            170            175
Gly Gly Gly Asn Val Ser Ile Ile Val Leu Gly Gly Ala Lys Glu Ala
      180            185            190

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Leu	Glu	Ala	His	Pro	Gly	Thr	Phe	Thr	Leu	Cys	Ile	Arg	Gln	Arg	Lys
		195					200					205			
Gly	Phe	Val	Lys	Met	Ala	Leu	Thr	His	Gly	Ala	Ser	Leu	Val	Pro	Val
	210					215				220					
Phe	Ser	Phe	Gly	Glu	Asn	Asp	Leu	Tyr	Lys	Gln	Ile	Asn	Asn	Pro	Lys
225					230					235					240
Gly	Ser	Trp	Leu	Arg	Thr	Ile	Gln	Asp	Ala	Met	Tyr	Asp	Ser	Met	Gly
				245						250				255	
Val	Ala	Leu	Pro	Leu	Ile	Tyr	Ala	Arg	Gly	Ile	Phe	Gln	His	Tyr	Phe
			260					265					270		
Gly	Ile	Met	Pro	Tyr	Arg	Lys	Leu	Ile	Tyr	Thr	Val	Val	Gly	Arg	Pro
		275						280					285		
Ile	Pro	Val	Gln	Gln	Ile	Leu	Asn	Pro	Thr	Ser	Glu	Gln	Ile	Glu	Glu
		290					295					300			
Leu	His	Gln	Thr	Tyr	Leu	Glu	Glu	Leu	Lys	Lys	Leu	Phe	Asn	Glu	His
305						310				315					320
Lys	Gly	Lys	Tyr	Gly	Ile	Pro	Glu	His	Glu	Thr	Leu	Val	Phe	Lys	
				325					330					335	

<210> 7
 <211> 1129
 <212> DNA
 <213> Homo sapiens

<400> 7

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gtcctttctt	ttcttacagg	gccgatgtcc	attggaatca	ctgtgatgct	gatcatacac	180
aactatttgt	tcctttacat	cccttatttg	atgtggcttt	actttgactg	gcatacccca	240
gagcgaggag	gcaggagatc	cagctggatc	aaaaattgga	ctctttggaa	acactttaag	300
gactattttc	caattcatct	tatcaaaact	caagatttgg	atccaagtca	caactatata	360
tttgggtttc	acccccatgg	aataatggca	gttggagcct	ttgggaattt	ttctgtaaat	420
tattctgact	tcaaggacct	gtttcctggc	tttacttcat	atcttcacgt	gctgccactt	480
tggttctggt	gtcctgtctt	tcgagaatat	gtgatgagtg	ttgggctggt	ttcagtttcc	540
aagaaaagtg	tgctctacat	ggtaagcaag	gagggaggtg	gaaacatctc	tgctattgtc	600
cttgggggtg	caaaagaatc	actggatgct	catcctggaa	agttcactct	gttcatccgc	660
cagcggaaag	gatttggtta	aattgctttg	acccatggcg	cctctctggt	cccagtgggt	720
tccttttggt	aaaatgaact	gtttaaacia	actgacaacc	ctgaaggatc	atggattaga	780
actgttcaga	ataaactgca	gaagatcatg	gggtttgctt	tgccctgtt	tcatgccagg	840
ggagtttttc	agtacaattt	tggcctaatt	acctatagga	aagccatcca	cactgttggt	900
ggccgcccga	tcctgtttcg	tcagactctg	aacccgaccc	aggagcagat	tgaggagtta	960
catcagacct	atatggagga	acttaggaaa	ttgtttgagg	aacacaaagg	aaagtatggc	1020
attccagagc	acgagactct	tgttttaaaa	tgacttgact	ataaaaaaaa	attaaaaaat	1080
aaaaataaat	gacttggctg	taataaggca	taaagaagga	taagagacc		1129

<210> 8
 <211> 334
 <212> PRT
 <213> Homo sapiens

<400> 8

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20      25      30
Met Ser Ile Gly Ile Thr Val Met Leu Ile Ile His Asn Tyr Leu Phe
35      40      45
Leu Tyr Ile Pro Tyr Leu Met Trp Leu Tyr Phe Asp Trp His Thr Pro
50      55      60
Glu Arg Gly Gly Arg Arg Ser Ser Trp Ile Lys Asn Trp Thr Leu Trp
65      70      75      80
Lys His Phe Lys Asp Tyr Phe Pro Ile His Leu Ile Lys Thr Gln Asp
85      90      95
Leu Asp Pro Ser His Asn Tyr Ile Phe Gly Phe His Pro His Gly Ile
100     105     110
Met Ala Val Gly Ala Phe Gly Asn Phe Ser Val Asn Tyr Ser Asp Phe
115     120     125
Lys Asp Leu Phe Pro Gly Phe Thr Ser Tyr Leu His Val Leu Pro Leu
130     135     140
Trp Phe Trp Cys Pro Val Phe Arg Glu Tyr Val Met Ser Val Gly Leu
145     150     155     160
Val Ser Val Ser Lys Lys Ser Val Ser Tyr Met Val Ser Lys Glu Gly
165     170     175
Gly Gly Asn Ile Ser Val Ile Val Leu Gly Gly Ala Lys Glu Ser Leu
180     185     190
Asp Ala His Pro Gly Lys Phe Thr Leu Phe Ile Arg Gln Arg Lys Gly
195     200     205
Phe Val Lys Ile Ala Leu Thr His Gly Ala Ser Leu Val Pro Val Val
210     215     220
Ser Phe Gly Glu Asn Glu Leu Phe Lys Gln Thr Asp Asn Pro Glu Gly
225     230     235     240
Ser Trp Ile Arg Thr Val Gln Asn Lys Leu Gln Lys Ile Met Gly Phe
245     250     255
Ala Leu Pro Leu Phe His Ala Arg Gly Val Phe Gln Tyr Asn Phe Gly
260     265     270
Leu Met Thr Tyr Arg Lys Ala Ile His Thr Val Val Gly Arg Pro Ile
275     280     285
Pro Val Arg Gln Thr Leu Asn Pro Thr Gln Glu Gln Ile Glu Glu Leu
290     295     300
His Gln Thr Tyr Met Glu Glu Leu Arg Lys Leu Phe Glu Glu His Lys
305     310     315     320
Gly Lys Tyr Gly Ile Pro Glu His Glu Thr Leu Val Leu Lys
325     330

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<210> 9
 <211> 435
 <212> DNA
 <213> Mus musculus

<220>
 <221> misc_feature
 <222> (1)...(435)

<223> n = A,T,C or G

<400> 9

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tgtaatttg cctattgttc acacccttgt ggccgctacc aacagtttac tttgtctggt      180
tacttctcga ctggaagact ccagataaag gtggcaggcg ttcagactgg gtacggaact      240
ggaatgtctg gaaccacatc agggactatt tccccattac aatcctgaag actaaggacc      300
tgtcaccttc agagaactac atcatggggg tccaccccat nggtctcctg accttcgggtg      360
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<210> 10

<211> 229

<212> PRT

<213> Mus musculus

<400> 10

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  20          25          30
Leu Phe Thr Pro Leu Trp Pro Leu Pro Thr Val Tyr Phe Val Trp Leu
  35          40          45
Leu Leu Asp Trp Lys Thr Pro Asp Lys Gly Gly Arg Arg Ser Asp Trp
  50          55          60
Val Arg Asn Trp Asn Val Trp Asn His Ile Arg Asp Tyr Phe Pro Ile
  65          70          75          80
Thr Ile Leu Lys Thr Lys Asp Leu Ser Pro Ser Glu Asn Tyr Ile Met
  85          90          95
Gly Val His Pro His Gly Leu Leu Thr Phe Gly Ala Phe Cys Asn Phe
  100          105          110
Cys Thr Glu Ala Thr Gly Phe Ser Lys Thr Phe Pro Gly Ile Thr Pro
  115          120          125
His Leu Ala Thr Leu Ser Trp Phe Phe Lys Ile Pro Ile Ile Arg Asp
  130          135          140
Tyr Ile Met Ala Lys Gly Leu Cys Ser Val Ser Gln Ala Ser Ile Asp
  145          150          155          160
Tyr Leu Leu Ser His Gly Thr Gly Asn Leu Val Gly Ile Pro Ile Ile
  165          170          175
Thr Val Val Gly Glu Ala Leu Pro Leu Pro Gln Val Lys Asn Pro Ser
  180          185          190
Pro Glu Ile Val Asp Lys Tyr His Ala Leu Tyr Met Asp Ala Leu Tyr
  195          200          205
Lys Leu Phe Glu Gln His Lys Val Gln Tyr Gly Cys Ser Asn Thr Gln
  210          215          220
Lys Leu Ile Phe Leu
225
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<210> 11

<211> 1240

<212> DNA
<213> Homo sapiens

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gttttgcaat ggatcccagt ctatatattt ttagtttgga tcttgccagcc attgttcgtc 180
tacctgctgt ttacatcctt gtggccgcta ccagtgtttt actttgcctg gttgttcctg 240
gactggaaga ccccagagcg aggtggcagg cgttcggcct gggtaaggaa ctgggtgtgtc 300
tggaccacaca tcagggacta tttcccatt acgatcctga agacaaagga cctatcacct 360
gagcacaact acctcatggg gggtcacccc catggcctcc tgaccttttg cgccttctgc 420
aacttctgca ctgaggccac aggccttctg aagaccttcc caggcatcac tctcacttg 480
gccacgctgt cctggtttctt caagatcccc tttgttaggg agtacctcat ggccaaagg 540
gtgtgctctg tgagccagcc agccatcaac tatctgctga gccatggcac tggcaacctc 600
gtgggcattg tagtgggagg tgtgggtgag gccctgcaaa gtgtgcccac caccaccacc 660
ctcatcctcc agaagcgcaa ggggttcgtg cgcacagccc tccagcatgg ggcatacctt 720
gtcccttcat attccttttg tgagaacgaa gttttcaatc aggagacctt ccctgagggc 780
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aatttctgta ccttccatgg ccggggcttc actcgcggat cctgggggctt cctgcctttc 900
aatcgcccca ttaccactgt tgttggggaa ccccttccaa tcccaggat taagaggcca 960
aaccagaaga cagtagacaa gtatcacgca ctctacatca gtgccctgcg caagctcttt 1020
gaccaacaca aagttgaata tggcctccct gagacccaag agctgacaat tacataacag 1080
gagccacatt ccccatgat caacccccaa agccatgagg gatccaagta gagccacaga 1140
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agaaattatt taataaatca gagttctagc aatagagtcc 1240

<210> 12
<211> 335
<212> PRT
<213> Homo sapiens

<400> 12
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Phe Val Leu Gln Trp Ile Pro Val Tyr Ile Phe Leu Val Trp Ile Leu
20 25 30
Gln Pro Leu Phe Val Tyr Leu Leu Phe Thr Ser Leu Trp Pro Leu Pro
35 40 45
Val Leu Tyr Phe Ala Trp Leu Phe Leu Asp Trp Lys Thr Pro Glu Arg
50 55 60
Gly Gly Arg Arg Ser Ala Trp Val Arg Asn Trp Cys Val Trp Thr His
65 70 75 80
Ile Arg Asp Tyr Phe Pro Ile Thr Ile Leu Lys Thr Lys Asp Leu Ser
85 90 95
Pro Glu His Asn Tyr Leu Met Gly Val His Pro His Gly Leu Leu Thr
100 105 110
Phe Gly Ala Phe Cys Asn Phe Cys Thr Glu Ala Thr Gly Phe Ser Lys
115 120 125
Thr Phe Pro Gly Ile Thr Pro His Leu Ala Thr Leu Ser Trp Phe Phe
130 135 140
Lys Ile Pro Phe Val Arg Glu Tyr Leu Met Ala Lys Gly Val Cys Ser

145		150		155		160
Val Ser Gln Pro Ala Ile Asn Tyr Leu Leu Ser His Gly Thr Gly Asn						
	165		170		175	
Leu Val Gly Ile Val Val Gly Gly Val Gly Glu Ala Leu Gln Ser Val						
	180		185		190	
Pro Asn Thr Thr Thr Leu Ile Leu Gln Lys Arg Lys Gly Phe Val Arg						
	195		200		205	
Thr Ala Leu Gln His Gly Ala Tyr Leu Val Pro Ser Tyr Ser Phe Gly						
	210		215		220	
Glu Asn Glu Val Phe Asn Gln Glu Thr Phe Pro Glu Gly Thr Trp Leu						
	225		230		235	240
Arg Leu Phe Gln Lys Thr Phe Gln Asp Thr Phe Lys Lys Ile Leu Gly						
	245		250		255	
Leu Asn Phe Cys Thr Phe His Gly Arg Gly Phe Thr Arg Gly Ser Trp						
	260		265		270	
Gly Phe Leu Pro Phe Asn Arg Pro Ile Thr Thr Val Val Gly Glu Pro						
	275		280		285	
Leu Pro Ile Pro Arg Ile Lys Arg Pro Asn Gln Lys Thr Val Asp Lys						
	290		295		300	
Tyr His Ala Leu Tyr Ile Ser Ala Leu Arg Lys Leu Phe Asp Gln His						
	305		310		315	320
Lys Val Glu Tyr Gly Leu Pro Glu Thr Gln Glu Leu Thr Ile Thr						
	325		330		335	

<210> 13
 <211> 1872
 <212> DNA
 <213> Homo sapiens

<400> 13

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tttctccagt	ctttcaggtc	ccttcaccag	ggaaccatta	acttgtgcat	cagaacaagg	240
acatttccct	acatttctgc	aaacacagtc	ctttcagttt	actctttttt	tgaggggggg	300
gcgcggggaa	cggagtctcg	ctctgtcgcc	caggctggag	tgcaatggtg	caatctcagc	360
tcaactgcaac	ctctgcctcc	caggtccaag	cgatttcctc	gcctcagcct	cccgggtagc	420
cgggactaca	ggcgctgcc	accacgccc	gctaattttt	gtatttttag	tagagacgag	480
gtttcgccgt	gttggcaggc	tggtcttgga	actcctgacc	tcaggtgatt	tactcgcttc	540
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gctcatttgt	catctatgcc	agagaagatt	tggagaggag	gacgtgaatt	ggaggaaaac	720
tgttccagga	ttccccacct	ctgggtggcc	accgctggct	cactgccatt	gaccacactg	780
caggcagagc	ctagtgcagt	gctggagcag	ggcccagaga	ggagagggct	tacagtgtga	840
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aaccactgtg	attgtgttca	acctctacct	gggtgtgttc	acaccatact	ggcctgtcac	960
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gatatttctt	ggcatcaccc	cttacatact	cacactggga	gcctttttct	ggatgccttt	1260

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cctcagagaa tatgtaatgt ctacaggggc ctgctctgtg agtcgatacct ccattgactt 1320
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gtgcagatac agcctgccag gttctttctac cctgggtgttg aagaaccggg ctggctttgt 1440
gcgcatggcc cttcagcatg gggtgccctct aatacctgcc tatgcctttg gggagacgga 1500
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ccagagcatg gtacacatct acccttgtgc tttctatgga cgtggcttca ccaagaactc 1620
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gccaagatt gagaatccaa gccaggagat cgtgggctaaa tatcacacac tctatattga 1740
tgccctacgt aaactgtttg accagcataa gaccaagttt ggtatctcag agaccagga 1800
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gaccagtga ga 1872

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<210> 14
<211> 333
<212> PRT
<213> Homo sapiens

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<400> 14
Met Leu Leu Pro Ser Lys Lys Asp Leu Lys Thr Ala Leu Asp Val Phe
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Ala Val Phe Gln Trp Ser Phe Ser Ala Leu Leu Ile Thr Thr Thr Val
             20             25             30
Ile Ala Val Asn Leu Tyr Leu Val Val Phe Thr Pro Tyr Trp Pro Val
             35             40             45
Thr Val Leu Ile Leu Thr Trp Leu Ala Phe Asp Trp Lys Thr Pro Gln
             50             55             60
Arg Gly Gly Arg Arg Phe Thr Cys Val Arg His Trp Arg Leu Trp Lys
             65             70             75             80
His Tyr Ser Asp Tyr Phe Pro Leu Lys Leu Leu Lys Thr His Asp Ile
             85             90             95
Cys Pro Ser Arg Asn Tyr Ile Leu Val Cys His Pro His Gly Leu Phe
             100            105            110
Ala His Gly Trp Phe Gly His Phe Ala Thr Glu Ala Ser Gly Phe Ser
             115            120            125
Lys Ile Phe Pro Gly Ile Thr Pro Tyr Ile Leu Thr Leu Gly Ala Phe
             130            135            140
Phe Trp Met Pro Phe Leu Arg Glu Tyr Val Met Ser Thr Gly Ala Cys
             145            150            155            160
Ser Val Ser Arg Ser Ser Ile Asp Phe Leu Leu Thr His Lys Gly Thr
             165            170            175
Gly Asn Met Val Ile Val Val Ile Gly Gly Leu Ala Glu Cys Arg Tyr
             180            185            190
Ser Leu Pro Gly Ser Ser Thr Leu Val Leu Lys Asn Arg Ser Gly Phe
             195            200            205
Val Arg Met Ala Leu Gln His Gly Val Pro Leu Ile Pro Ala Tyr Ala
             210            215            220
Phe Gly Glu Thr Asp Leu Tyr Asp Gln His Ile Phe Thr Pro Gly Gly
             225            230            235            240
Phe Val Asn Arg Phe Gln Lys Trp Phe Gln Ser Met Val His Ile Tyr
             245            250            255
Pro Cys Ala Phe Tyr Gly Arg Gly Phe Thr Lys Asn Ser Trp Gly Leu

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	260		265		270										
Leu	Pro	Tyr	Ser	Arg	Pro	Val	Thr	Thr	Ile	Val	Gly	Glu	Pro	Leu	Pro
	275						280				285				
Met	Pro	Lys	Ile	Glu	Asn	Pro	Ser	Gln	Glu	Ile	Val	Ala	Lys	Tyr	His
	290						295				300				
Thr	Leu	Tyr	Ile	Asp	Ala	Leu	Arg	Lys	Leu	Phe	Asp	Gln	His	Lys	Thr
305					310					315					320
Lys	Phe	Gly	Ile	Ser	Glu	Thr	Gln	Glu	Leu	Glu	Ile	Ile			
			325					330							

<210> 15
 <211> 1050
 <212> DNA
 <213> Homo sapiens

<400> 15

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ttctccttct	tggcactggg	taagatctgc	actgtgggct	tcatagccct	cctgtttaca	180
agattctggc	tcctcactgt	cctgtatgcg	gctgtgtggg	atctggaccg	agacaagcca	240
cggcaggggg	gccggcacat	ccaggccatc	agggtgctga	ctatatggaa	gtacatgaag	300
gactatttcc	ccatccagct	ggtcaagact	gctgagctgg	acccctctcg	gaactacatt	360
gcgggcttcc	accccatgg	agtcctggca	gtcggagcct	ttgccaacct	gtgcaactgag	420
agcacaggct	tctcttcgat	cttccccggt	atccgcccc	atctgatgat	gctgaccttg	480
tggttccggg	cccccttctt	cagagattac	atcatgtctg	cagggttggt	cacatcagaa	540
aaggagagtg	ctgctcacat	tctgaacagg	aagggtggcg	gaaacttgct	gggcatcatt	600
gtaggggggtg	cccaggaggc	cctggatgcc	aggcctggat	ccttcacgct	gttactgcgg	660
aaccgaaagg	gcttcgtcag	gctcgccctg	acacacgggg	cacccctggg	gccaatcttc	720
tccttcgggg	agaatgacct	atttgaccag	attcccaact	cttctggctc	ctggttacgc	780
tatatccaga	atcggttgca	gaagatcatg	ggcatctccc	tcccactctt	tcattggccgt	840
ggtgtcttcc	agtagagctt	tggtttaata	ccctaccgcc	ggcccatcac	cactgtgggg	900
aagcccatcg	aggtacagaa	gacgtgcat	ccctcggagg	aggaggtgaa	ccagctgcac	960
cagcattata	tcaaagagct	gtgcaacctc	ttcgaggccc	acaaacttaa	gttcaacatc	1020
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<210> 16
 <211> 333
 <212> PRT
 <213> Homo sapiens

<400> 16

Met	Val	Glu	Phe	Ala	Pro	Leu	Phe	Val	Pro	Trp	Glu	Arg	Arg	Leu	Gln
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Thr	Leu	Ala	Val	Leu	Gln	Phe	Val	Phe	Ser	Phe	Leu	Ala	Leu	Gly	Lys
			20					25					30		
Ile	Cys	Thr	Val	Gly	Phe	Ile	Ala	Leu	Leu	Phe	Thr	Arg	Phe	Trp	Leu
		35					40				45				
Leu	Thr	Val	Leu	Tyr	Ala	Ala	Trp	Trp	Tyr	Leu	Asp	Arg	Asp	Lys	Pro
	50					55				60					
Arg	Gln	Gly	Gly	Arg	His	Ile	Gln	Ala	Ile	Arg	Cys	Trp	Thr	Ile	Trp
65					70					75				80	

Lys Tyr Met Lys Asp Tyr Phe Pro Ile Gln Leu Val Lys Thr Ala Glu
85 90 95
Leu Asp Pro Ser Arg Asn Tyr Ile Ala Gly Phe His Pro His Gly Val
100 105 110
Leu Ala Val Gly Ala Phe Ala Asn Leu Cys Thr Glu Ser Thr Gly Phe
115 120 125
Ser Ser Ile Phe Pro Gly Ile Arg Pro His Leu Met Met Leu Thr Leu
130 135 140
Trp Phe Arg Ala Pro Phe Phe Arg Asp Tyr Ile Met Ser Ala Gly Leu
145 150 155 160
Val Thr Ser Glu Lys Glu Ser Ala Ala His Ile Leu Asn Arg Lys Gly
165 170 175
Gly Gly Asn Leu Leu Gly Ile Ile Val Gly Gly Ala Gln Glu Ala Leu
180 185 190
Asp Ala Arg Pro Gly Ser Phe Thr Leu Leu Leu Arg Asn Arg Lys Gly
195 200 205
Phe Val Arg Leu Ala Leu Thr His Gly Ala Pro Leu Val Pro Ile Phe
210 215 220
Ser Phe Gly Glu Asn Asp Leu Phe Asp Gln Ile Pro Asn Ser Ser Gly
225 230 235 240
Ser Trp Leu Arg Tyr Ile Gln Asn Arg Leu Gln Lys Ile Met Gly Ile
245 250 255
Ser Leu Pro Leu Phe His Gly Arg Gly Val Phe Gln Tyr Ser Phe Gly
260 265 270
Leu Ile Pro Tyr Arg Arg Pro Ile Thr Thr Val Gly Lys Pro Ile Glu
275 280 285
Val Gln Lys Thr Leu His Pro Ser Glu Glu Glu Val Asn Gln Leu His
290 295 300
Gln His Tyr Ile Lys Glu Leu Cys Asn Leu Phe Glu Ala His Lys Leu
305 310 315 320
Lys Phe Asn Ile Pro Ala Asp Gln His Leu Glu Phe Cys
325 330

<210> 17
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic peptide

<400> 17
Met Gly Asp Tyr Lys Asp Asp Asp Asp Gly
1 5 10

<210> 18
<211> 1233
<212> DNA
<213> Homo sapiens

<400> 18

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gagatggggc	actggatcca	gcatcctctc	cgccctccag	gacctcttct	ctgtcacctg	180
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gtccttcctt	gtactgggag	tggcctgcag	tgccatcctc	atgtacatat	tctgcaactga	300
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gaaaggtggc	aggaggtcac	agtgggtccg	aaactgggct	gtgtggcgct	actttcgaga	420
ctactttccc	atccagctgg	tgaagacaca	caacctgctg	accaccagga	actatatctt	480
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cacagaagtg	agcaagaagt	tcccaggcat	acggccttac	ctggctacac	tggcaggcaa	600
cttccgaatg	cctgtgttga	gggagtacct	gatgtctgga	ggtatctgcc	ctgtcagccg	660
ggacaccata	gactatttgc	tttcaaagaa	tgggagtggc	aatgctatca	tcacgtgggt	720
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ccgcaagggc	tttgtgaaac	tggccctgcg	tcatggagct	gacctggttc	ccatctactc	840
ctttggagag	aatgaagtgt	acaagcaggt	gatcttcgag	gagggctcct	ggggccgatg	900
ggtccagaag	aagttccaga	aatacattgg	tttcgcccc	tgcattctcc	atggctgagg	960
cctcttctcc	tccgacacct	gggggctggt	gccctactcc	aagcccatca	ccactgttgt	1020
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